

Resource Summary Report

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[easyRNASeq](#)

RRID:SCR_012020

Type: Tool

Proper Citation

easyRNASeq (RRID:SCR_012020)

Resource Information

URL: <http://www.bioconductor.org/packages/2.11/bioc/html/easyRNASeq.html>

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Description: Software that calculates the coverage of high-throughput short-reads against a genome of reference and summarizes it per feature of interest (e.g. exon, gene, transcript). The data can be normalized as "RPKM" or by the "DESeq" or "edgeR" package.

Abbreviations: easyRNASeq

Synonyms: easyRNASeq - Count summarization and normalization for RNA-Seq data

Resource Type: software resource

Defining Citation: [PMID:22847932](#)

Keywords: rna-seq, gene expression, genetics, preprocessing, bio.tools

Availability: Artistic License, v2

Resource Name: easyRNASeq

Resource ID: SCR_012020

Alternate IDs: OMICS_01938, biotools:easyrnaseq

Alternate URLs: <https://bio.tools/easyrnaseq>

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260725T190726+0000

Ratings and Alerts

No rating or validation information has been found for easyRNASeq.

No alerts have been found for easyRNASeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Saenz C, et al. (2025) Muscle transcriptome profiles in elite male ultra-endurance athletes acclimated to a high-carbohydrate versus low-carbohydrate diet. Scientific reports, 15(1), 8419.

Mora P, et al. (2024) Sex-biased gene content is associated with sex chromosome turnover in Danaini butterflies. Molecular ecology, 33(24), e17256.

Pal J, et al. (2021) Systematic analysis of migration factors by MigExpress identifies essential cell migration control genes in non-small cell lung cancer. Molecular oncology, 15(7), 1797.

Zhang M, et al. (2021) Identification of Differentially Expressed Genes and Lipid Metabolism Signaling Pathways between Muscle and Fat Tissues in Broiler Chickens. The journal of poultry science, 58(2), 131.

Newell NR, et al. (2020) The Drosophila Post-mating Response: Gene Expression and Behavioral Changes Reveal Perdurance and Variation in Cross-Tissue Interactions. G3 (Bethesda, Md.), 10(3), 967.

Liu W, et al. (2020) Identification of lncRNA-associated differential subnetworks in oesophageal squamous cell carcinoma by differential co-expression analysis. Journal of cellular and molecular medicine, 24(8), 4804.

Mola S, et al. (2020) A transcriptome-based approach to identify functional modules within and across primary human immune cells. PloS one, 15(5), e0233543.

Bray ER, et al. (2019) Thrombospondin-1 Mediates Axon Regeneration in Retinal Ganglion Cells. Neuron, 103(4), 642.

Cocce KJ, et al. (2019) The Lineage Determining Factor GRHL2 Collaborates with FOXA1 to Establish a Targetable Pathway in Endocrine Therapy-Resistant Breast Cancer. Cell reports, 29(4), 889.

Hans CP, et al. (2019) Transcriptomics Analysis Reveals New Insights into the Roles of Notch1 Signaling on Macrophage Polarization. Scientific reports, 9(1), 7999.

Bundy JL, et al. (2019) Sex-biased hippocampal pathology in the 5XFAD mouse model of Alzheimer's disease: A multi-omic analysis. *The Journal of comparative neurology*, 527(2), 462.

Nordquist E, et al. (2018) Postnatal and Adult Aortic Heart Valves Have Distinctive Transcriptional Profiles Associated With Valve Tissue Growth and Maintenance Respectively. *Frontiers in cardiovascular medicine*, 5, 30.

Bundy JL, et al. (2017) Sex differences in the molecular signature of the developing mouse hippocampus. *BMC genomics*, 18(1), 237.

Piras IS, et al. (2017) Whole transcriptome profiling of the human hippocampus suggests an involvement of the KIBRA rs17070145 polymorphism in differential activation of the MAPK signaling pathway. *Hippocampus*, 27(7), 784.

Chen J, et al. (2017) A systems-level approach reveals new gene regulatory modules in the developing ear. *Development (Cambridge, England)*, 144(8), 1531.

Li CQ, et al. (2017) Integrative analyses of transcriptome sequencing identify novel functional lncRNAs in esophageal squamous cell carcinoma. *Oncogenesis*, 6(2), e297.

DiCarlo LM, et al. (2017) The stability of the transcriptome during the estrous cycle in four regions of the mouse brain. *The Journal of comparative neurology*, 525(15), 3360.

Jones BC, et al. (2016) A somatic piRNA pathway in the *Drosophila* fat body ensures metabolic homeostasis and normal lifespan. *Nature communications*, 7, 13856.

D'Argenio V, et al. (2016) The complete 12 Mb genome and transcriptome of *Nonomuraea gerenzanensis* with new insights into its duplicated "magic" RNA polymerase. *Scientific reports*, 6(1), 18.

Xing K, et al. (2016) Identification of genes for controlling swine adipose deposition by integrating transcriptome, whole-genome resequencing, and quantitative trait loci data. *Scientific reports*, 6, 23219.